

CLAIMS

What is claimed is:

1. An isolated nucleic acid fragment encoding a dehydroquinase/shikimate dehydrogenase comprising a member selected from the group consisting of:

5 (a) an isolated nucleic acid fragment encoding an amino acid sequence that is at least 80% identical to the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8;

(b) an isolated nucleic acid fragment that is complementary to (a).

10 2. The isolated nucleic acid fragment of Claim 1 wherein nucleic acid fragment is a functional RNA.

3. The isolated nucleic acid fragment of Claim 1 wherein the nucleotide sequence of the fragment comprises the sequence set forth in a member selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7.

15 4. A chimeric gene comprising the nucleic acid fragment of Claim 1 operably linked to suitable regulatory sequences.

5. A transformed host cell comprising the chimeric gene of Claim 4.

6. An isolated nucleic acid fragment encoding a shikimate kinase comprising a member selected from the group consisting of:

20 (a) an isolated nucleic acid fragment comprising at least 400 nucleotides wherein the nucleic acid fragment encodes an amino acid sequence that is at least 80% identical to the amino acid sequence set forth in a member selected from the group consisting of SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID  
25 NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26 and SEQ ID NO:28;

(b) an isolated nucleic acid fragment that is complementary to (a).

7. The isolated nucleic acid fragment of Claim 6 wherein nucleic acid fragment is a functional RNA.

30 8. The isolated nucleic acid fragment of Claim 6 wherein the nucleotide sequence of the fragment comprises the sequence set forth in a member selected from the group consisting of SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25 and SEQ ID NO:27.

35 9. A chimeric gene comprising the nucleic acid fragment of Claim 6 operably linked to suitable regulatory sequences.

10. A transformed host cell comprising the chimeric gene of Claim 9.

11. A method for evaluating at least one compound for its ability to inhibit the activity of a chorismate biosynthetic enzyme, the method comprising the steps of:

- 5 (a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a chorismate biosynthetic enzyme, operably linked to suitable regulatory sequences;
- (b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the chorismate biosynthetic enzyme encoded by the operably linked nucleic acid fragment in the  
10 transformed host cell;
- (c) optionally purifying the chorismate biosynthetic enzyme expressed by the transformed host cell;
- (d) treating the chorismate biosynthetic enzyme with a compound to be tested; and
- 15 (e) comparing the activity of the chorismate biosynthetic enzyme that has been treated with a test compound to the activity of an untreated chorismate biosynthetic enzyme,

thereby selecting compounds with potential for inhibitory activity.